

## **New Technology for Proteomics and Glycomics**

NOTE: The Solicitations and topics listed on this site are copies from the various SBIR agency solicitations and are not necessarily the latest and most up-to-date. For this reason, you should use the agency link listed below which will take you directly to the appropriate agency server where you can read the official version of this solicitation and download the appropriate forms and rules.

The official link for this solicitation is: <http://grants.nih.gov/grants/guide/pa-files/PA-11-215.html>

Agency:

Department of Health and Human Services

Release Date:

May 19, 2011

Branch:

n/a

Open Date:

May 19, 2011

Program / Phase / Year:

SBIR / Phase I / 2011

Application Due Date:

May 08, 2014

Solicitation:

[PA-11-215](#)

Close Date:

May 08, 2014

Topic Number:

PA-11-215

Description:

### **1. Research Objectives**

Proteomics continues to be a rapidly expanding field. However, despite explosive growth in both academic and commercial efforts, concrete technical capabilities are far from adequate to realize this promise. Proteomics technologies and methods in the three broad, interacting domains of biology, analytical chemistry, and informatics are still largely inadequate to address the bulk of challenging biological problems. This is the case with respect to both core capabilities and scale.

The broad scope of proteomics can be broken down into six types of questions that are addressed in some form: (1) identification of individual proteins, (2) recognition of protein interactions, (3) relative quantitation to distinguish differential expression of proteins, (4) characterization of post-translational modifications, (5) qualitative or quantitative measurements at high spatial and/or temporal resolution to address the dynamics of protein interactions, and (6) formulation of models based on results from components 1-5.

The categories above define the type of information being sought, and imply the need for technologies capable of addressing the challenges inherent in each type of experiment. Those specific technologies may reside within any of the three domains that define proteomics, or may function as a bridge between them. For example, tools for tissue or subcellular fractionation may reside squarely in the biological domain, but could also be designed in such a way as to maximize

synergy with widely used analytical separations methods. It is important that in a field as complex and interdisciplinary as proteomics, technology development be pursued with a sound understanding of context. One area of particular interest is the development of technologies that will permit observations to be quantitative and made in real time, whether for clinical studies or experimental systems.

In addition to the development of broadly applicable research tools that address the core technical challenges in proteomics, unique constraints in two subordinate areas merit special attention. We especially encourage applications in response to this announcement that address the unique needs of glycomics and clinical proteomics, described below.

The application of proteomics tools in the clinical setting lags far behind their use in basic science and drug discovery. Though this is not due solely to technological constraints, the unique challenges associated with development of simple, rapid, and robust technologies for the clinic demand a somewhat different perspective than might be taken in consideration of a purely research-driven project. Likewise, this difference in perspective and priorities should open the possibility of approaches that might be wholly inadequate from a research perspective but may be appropriate in the clinic. Finally, the exploitation of insights previously developed in research-oriented proteomics to develop more specific, robust tools for clinical applications is also an appropriate goal.

The complexity and diversity of glycosylation significantly complicates the linkage between genetic sequence and mature, active proteins. Glycobiology-focused proteomics, or glycomics, requires the development of novel approaches and tools directed at the special challenges of glycobiology. Among post-translational modifications, glycosylation is the only one that requires structural characterization of the modifying moiety beyond noting its presence. Strategies for separation, profiling, quantitation, and detailed characterization of carbohydrate structures are central challenges. Informatics tools are needed for data handling and reduction, correlation of carbohydrate and protein information, and a variety of other purposes. Discovery-based analytical tools that can survey the complexities of glycosylation on a system-wide basis may have significant biological impact.

The goals of this program announcement are deliberately discussed with respect to fundamental challenges, rather than in relation to specific technologies, in order to emphasize the overriding importance of surmounting obstacles, irrespective of the analytical strategy adopted to pursue those solutions. This solicitation is open to unconventional or alternative approaches.

See [Section VIII, Other Information - Required Federal Citations](#), for policies related to this announcement.